

WE CLAIM:

1. A method of modifying the endogenous oil of a cotton plant comprising producing a transgenic cotton plant having a gene construct which comprises a nucleotide sequence of a fatty acid biosynthesis gene or a gene fragment thereof operably in connection with a promoter sequence capable of conferring expression of said gene or gene fragment in the seed of a cotton plant, and wherein said fatty acid biosynthesis gene is selected from the group consisting of fatty acid $\Delta 9$ -desaturase ($\Delta 9$ stearoyl-ACP desaturase) genes, and fatty acid $\Delta 12$ -desaturase (Oleoyl-PC $\Delta 12$ -desaturase) genes.
2. The method according to claim 1 wherein the gene construct comprises a fatty acid biosynthesis gene or a gene fragment thereof which comprises a nucleotide sequence selected from the group consisting of:
 - (i) the nucleotide sequence set forth in SEQ ID NO: 1 or a fragment thereof;
 - (ii) a nucleotide sequence which encodes the amino acid sequence set forth in SEQ ID NO: 2 or a fragment thereof;
 - (iii) a nucleotide sequence which is complementary to (i) or (ii); and
 - (iv) an inverted repeat sequence having self-complementarity and consisting of a nucleotide sequence selected from the group consisting of:
 - (a) the nucleotide sequence of (i) linked to the nucleotide sequence of (iii); and
 - (b) the nucleotide sequence of (ii) linked to the nucleotide sequence of (iii);
3. The method according to claim 2 wherein the gene construct comprises the coding region of the nucleotide sequence set forth in SEQ ID NO: 1 or a fragment thereof in the antisense orientation.

4. The method according to claim 2 wherein the gene construct comprises an inverted repeat sequence of the 5'-terminal end of SEQ ID NO: 1 having self-complementarity.
5. The method according to claim 1 wherein the gene construct comprises a fatty acid biosynthesis gene or a gene fragment thereof which comprises a nucleotide sequence selected from the group consisting of:
- (i) the nucleotide sequence set forth in SEQ ID NO: 3 or SEQ ID NO: 7 or a fragment thereof;
 - (ii) a nucleotide sequence which encodes the amino acid sequence set forth in SEQ ID NO: 4 or a fragment thereof;
 - (iii) a nucleotide sequence which is complementary to (i) or (ii); and
 - (iv) an inverted repeat sequence having self-complementarity and consisting of a nucleotide sequence selected from the group consisting of:
 - (a) the nucleotide sequence of (i) linked to the nucleotide sequence of (iii); and
 - (b) the nucleotide sequence of (ii) linked to the nucleotide sequence of (iii).
6. The method according to claim 5 wherein the gene construct comprises the coding region of the nucleotide sequence set forth in SEQ ID NO: 3 or a fragment thereof in the antisense orientation.
7. The method according to claim 5 wherein the gene construct comprises an inverted repeat sequence of the 5'-terminal end of SEQ ID NO: 3 having self-complementarity or an inverted repeat of the 5'-untranslated region of the *ghFAD2-1* gene set forth in SEQ ID NO: 7 having self-complementarity.
8. The method according to claim 1, wherein the promoter is the soybean lectin promoter sequence or the *ghFAD2-1* gene promoter.

9. The method according to claim 1 wherein the gene construct is capable of being expressed in the cotton seed so as to reduce the level of expression of an endogenous cotton fatty acid biosynthesis gene to a level that is sufficient to modify the content and/or composition of the oil produced in said seed.
10. A transgenic cotton plant produced by the method according to claim 1 and having a modified level of cotton fatty acid $\Delta 9$ -desaturase ($\Delta 9$ stearoyl-ACP desaturase) in the seed compared to an isogenic non-transformed plant, or having a modified level of cotton fatty acid $\Delta 12$ -desaturase (Oleoyl-PC $\Delta 12$ -desaturase) in the seed compared to an isogenic non-transformed plant.
11. A cotton plant consisting of the progeny of the plant according to claim 10, wherein said progeny comprises the introduced fatty acid biosynthesis gene or gene fragment.
12. The cotton plant of claim 11 wherein said cotton plant has a modified level of cotton fatty acid $\Delta 9$ -desaturase ($\Delta 9$ stearoyl-ACP desaturase) in the seed compared to an isogenic non-transformed plant, or having a modified level of cotton fatty acid $\Delta 12$ -desaturase (Oleoyl-PC $\Delta 12$ -desaturase) in the seed compared to an isogenic non-transformed plant.
13. A seed of the cotton plant according to claim 10.
14. A method of modifying the endogenous oil of a cotton plant comprising:
(i) producing a transgenic cotton plant having a gene construct which comprises a nucleotide sequence of a fatty acid biosynthesis gene or a gene fragment thereof operably in connection with a promoter sequence capable of conferring expression of said gene or gene fragment in the seed of a cotton plant; and

(ii) growing said plant for a time and under conditions sufficient for the expression of the corresponding endogenous fatty acid biosynthesis gene to be reduced in the seed by virtue of the presence of said nucleotide sequence in its genome,

5 wherein said fatty acid biosynthesis gene is selected from the group consisting of fatty acid $\Delta 9$ -desaturase ($\Delta 9$ stearoyl-ACP desaturase) genes and fatty acid $\Delta 12$ -desaturase (Oleoyl-PC $\Delta 12$ -desaturase) genes.

10 15. The method according to claim 14 wherein the gene construct comprises a fatty acid biosynthesis gene or a gene fragment thereof which comprises a nucleotide sequence selected from the group consisting of:

- (i) the nucleotide sequence set forth in SEQ ID NO: 1 or a fragment thereof;
- (ii) a nucleotide sequence which encodes the amino acid sequence set forth in SEQ ID NO: 2 or a fragment thereof;
- (iii) a nucleotide sequence which is complementary to (i) or (ii); and
- (iv) an inverted repeat sequence having self-complementarity and consisting of a nucleotide sequence selected from the group consisting of:
 - 20 (a) the nucleotide sequence of (i) linked to the nucleotide sequence of (iii); and
 - (b) the nucleotide sequence of (ii) linked to the nucleotide sequence of (iii).

25 16. The method according to claim 15 wherein the gene construct comprises the coding region of the nucleotide sequence set forth in SEQ ID NO: 1 or a fragment thereof in the antisense orientation.

30 17. The method according to claim 15 wherein the gene construct comprises an inverted repeat sequence of the 5'-terminal end of SEQ ID NO:1 having self-complementarity.

18. A transgenic cotton plant produced by the method according to claim 15 and having a reduced level of palmitic acid in the seed compared to an isogenic non-transformed plant.
- 5 19. A transgenic cotton plant produced by the method according to claim 15 and having an increased level of stearic acid in the seed compared to an isogenic non-transformed plant.
- 10 20. A cotton plant consisting of the progeny of the plant according to claim 18, wherein said progeny has a decreased level of palmitic acid in the seed.
21. A cotton plant consisting of the progeny of the plant according to claim 19, wherein said progeny has an increased level of stearic acid in the seed.
- 15 22. A seed of the plant according to claim 19.
23. A seed of the plant according to claim 20.
- 20 24. The method according to claim 14 wherein the gene construct comprises a fatty acid biosynthesis gene or a gene-fragment thereof which comprises a nucleotide sequence selected from the group consisting of:
- 25 (i) the nucleotide sequence set forth in SEQ ID NO: 3 or SEQ ID NO: 7 or a fragment thereof;
- (ii) a nucleotide sequence which encodes the amino acid sequence set forth in SEQ ID NO:4 or a fragment thereof;
- (iii) a nucleotide sequence which is complementary to (i) or (ii); and
- (iv) an inverted repeat sequence having self-complementarity and consisting of a nucleotide sequence selected from the group consisting of:
- 30 (a) the nucleotide sequence of (i) linked to the nucleotide sequence of (iii); and

(b) the nucleotide sequence of (ii) linked to the nucleotide sequence of (iii).

25. The method according to claim 24 wherein the gene construct comprises
5 the coding region of the nucleotide sequence set forth in SEQ ID NO: 3 or a fragment thereof in the antisense orientation.
26. The method according to claim 24 wherein the gene construct comprises an
10 inverted repeat sequence of the 5'-terminal end of SEQ ID NO: 3 having self-complementarity or an inverted repeat of the 5'-untranslated region of the *ghFAD2-1* gene set forth in SEQ ID NO: 7 having self-complementarity.
27. A transgenic cotton plant produced by the method according to claim 24
15 and having a reduced level of palmitic acid in the seed compared to an isogenic non-transformed plant.
28. A transgenic cotton plant produced by the method according to claim 24
and having an increased level of oleic acid in the seed compared to an isogenic non-transformed plant.
29. A transgenic cotton plant produced by the method according to claim 24
20 and having a decreased level of linoleic acid in the seed compared to an isogenic non-transformed plant.
30. A cotton plant consisting of the progeny of the plant according to claim 27,
25 wherein said progeny has a decreased level of palmitic acid in the seed.
31. A cotton plant consisting of the progeny of the plant according to claim 28,
wherein said progeny has an increased level of oleic acid in the seed.
32. A cotton plant consisting of the progeny of the plant according to claim 29,
30 wherein said progeny has a decreased level of linoleic acid in the seed.

33. A seed of the plant according to claim 30.
34. A seed of the plant according to claim 31.
- 5 35. A seed of the plant according to claim 32.
36. The method according to claim 15 further comprising transforming the transgenic cotton plant or a cell of said plant with a second gene construct which comprises a nucleotide sequence of a fatty acid $\Delta 12$ -desaturase (Oleoyl-PC $\Delta 12$ -desaturase) gene or a gene fragment thereof placed operably in connection with a promoter sequence capable of conferring expression of said gene or gene fragment in the seed of a cotton plant for a time and under conditions sufficient to decrease the expression of the corresponding endogenous fatty acid $\Delta 12$ -desaturase (Oleoyl-PC $\Delta 12$ -desaturase) gene in the seed of said cotton plant.
- 10 37. The method according to claim 24 further comprising transforming the transgenic cotton plant or a cell of said plant with a second gene construct which comprises a nucleotide sequence of a fatty acid $\Delta 9$ -desaturase ($\Delta 9$ -stearoyl-ACP desaturase) gene or a gene fragment thereof placed operably in connection with a promoter sequence capable of conferring expression of said gene or gene fragment in the seed of a cotton plant for a time and under conditions sufficient to decrease the expression of the corresponding endogenous fatty acid $\Delta 9$ -desaturase ($\Delta 9$ -stearoyl-ACP desaturase) gene in the seed of said cotton plant.
- 15 20 25 38. A method of modifying the endogenous oil of a cotton plant comprising:
- 30 (i) producing a transgenic cotton plant having a gene construct that comprises a nucleotide sequence of a fatty acid $\Delta 9$ -desaturase ($\Delta 9$ -stearoyl-ACP desaturase) gene or a gene fragment thereof operably

in connection with a promoter sequence capable of conferring expression of said gene or gene fragment in the seed of a cotton plant, and growing said plant for a time and under conditions sufficient for the expression of the endogenous fatty acid $\Delta 9$ -desaturase ($\Delta 9$ stearoyl-ACP desaturase) gene in the seed to be reduced;

- (ii) producing a transgenic cotton plant having a gene construct that comprises a nucleotide sequence of a fatty acid $\Delta 12$ -desaturase (Oleoyl-PC $\Delta 12$ -desaturase) gene or a gene fragment thereof operably in connection with a promoter sequence capable of conferring expression of said gene or gene fragment in the seed of a cotton plant, and growing said plant for a time and under conditions sufficient for the expression of the endogenous fatty acid $\Delta 12$ -desaturase (Oleoyl-PC $\Delta 12$ -desaturase) gene in the seed to be reduced;
- (iii) crossing the cotton plant of (i) with the cotton plant of (ii); and
- (iv) selecting the progeny of said crossing wherein said progeny have modified fatty acid content compared to a nontransformed isogenic cotton plant.

39. A cotton plant produced by the method according to claim 38 and having a reduced level of palmitic acid or linoleic acid in the seed compared to an isogenic non-transformed plant.

40. A seed of the plant according to claim 39.

41. A cotton plant produced by the method according to claim 38 and having an increased level of stearic acid or oleic acid in the seed compared to an isogenic non-transformed plant.

42. A cotton plant produced by the method according to claim 38 and having increased levels of stearic acid and oleic acid in the seed compared to an isogenic non-transformed plant.
- 5 43. A seed of the plant according to claim 41.
44. A seed of the plant according to claim 42.
45. The method according to claim 38 wherein the transgenic cotton plant at (i) or (ii) is a progeny of a primary transformed plant.
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46. A cotton plant having increased oleic acid and stearic acid in the seed wherein said plant is produced by a process comprising sexual hybridisation between a first cotton plant having increased oleic acid in the seed compared to an isogenic non-transformed cotton plant and a second cotton plant having increased stearic acid in the seed compared to an isogenic non-transformed cotton plant, and wherein said first cotton plant or said second cotton plant is produced by the method according to claim 14.
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47. The cotton plant according to claim 46 wherein said plant has decreased palmitic acid or linoleic acid in the seed.
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48. A seed produced by the plant according to claim 46.
- 25 49. Cottonseed oil from a plant produced according to the method of claim 15, wherein said oil has a characteristic selected from the group consisting of:
- (i) a high stearic acid content;
 - (ii) a reduced oleic acid content;
 - (iii) a reduced palmitic acid content; and
 - (iv) a reduced linoleic acid content.
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50. Cottonseed oil from a plant produced according to the method of claim 24, wherein said oil has a characteristic selected from the group consisting of:
- (i) a high oleic acid content;
 - (ii) a reduced palmitic acid content; and
 - (iii) a reduced linoleic acid content.
51. Cottonseed oil from a plant produced according to the method of claim 38, wherein said oil has a characteristic selected from the group consisting of:
- (i) a high oleic acid content;
 - (ii) a high stearic acid content;
 - (iii) a high stearic acid and a high oleic acid content;
 - (iv) a reduced palmitic acid content; and
 - (v) a reduced linoleic acid content.
52. Cottonseed oil from the plant according to claim 46, wherein said oil has a characteristic selected from the group consisting of:
- (i) a high oleic acid content;
 - (ii) a high stearic acid content;
 - (iii) a high stearic acid and a high oleic acid content;
 - (iv) a reduced palmitic acid content; and
 - (v) a reduced linoleic acid content.
53. A gene construct for modifying the fatty acid composition of cottonseed oil, comprising the nucleotide sequence of a plant fatty acid biosynthesis gene, or a gene fragment thereof, placed operably in connection with a promoter sequence that is operable in cotton seed, wherein said gene is selected from the group consisting of:
- (i) the nucleotide sequence set forth in SEQ ID NO: 1 or a fragment thereof;
 - (ii) a nucleotide sequence which encodes the amino acid sequence set forth in SEQ ID NO: 2 or a fragment thereof;

- (ii) the nucleotide sequence set forth in SEQ ID NO: 3 or SEQ ID NO: 7 or a fragment thereof;
- (iv) a nucleotide sequence which encodes the amino acid sequence set forth in SEQ ID NO: 4 or a fragment thereof;
- 5 (v) a nucleotide sequence which is complementary to any one of (i) to (iv);
- (vi) an inverted repeat sequence having self-complementarity and consisting of a nucleotide sequence selected from the group consisting of:
- 10 (a) the nucleotide sequence of (i) linked to the nucleotide sequence of (v);
- (b) the nucleotide sequence of (ii) linked to the nucleotide sequence of (v);
- (c) the nucleotide sequence of (iii) linked to the nucleotide sequence of (v); and
- 15 (d) the nucleotide sequence of (iv) linked to the nucleotide sequence of (v).
54. The gene construct according to claim 53 comprising the coding region of the nucleotide sequence set forth in SEQ ID NO: 1 or SEQ ID NO: 3 or a fragment thereof in the antisense orientation:
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55. The gene construct according to claim 53 comprising an inverted repeat sequence selected from the group consisting of:
- 25 (i) the 5'-terminal end of SEQ ID NO: 1 having self-complementarity;
- (ii) the 5'-terminal end of SEQ ID NO: 3 having self-complementarity; and
- (iii) the 5'-untranslated region of the *ghFAD2-1* gene set forth in SEQ ID NO: 7 having self-complementarity.
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56. The gene construct according to claim 53 wherein the promoter sequence is a soybean lectin gene promoter sequence or the *ghFAD2-1* gene promoter

57. The method of claim 2, wherein the inverted repeat is interrupted by an intervening sequence.
- 5 58. The method of claim 5, wherein the inverted repeat is interrupted by an intervening sequence.
59. The method of claim 15, wherein the inverted repeat is interrupted by an intervening sequence.
- 10 60. The method of claim 24, wherein the inverted repeat is interrupted by an intervening sequence.
- 15 61. The gene construct of claim 53 wherein the inverted repeat is interrupted by an intervening sequence.

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